MCP-1RA

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OM nucleic - nu	OM nucleic - nucleic search, using sw model
Run on:	June 1, 2003, 18:47:00; Search time 5614 Seconds (without alignments) 11570.620 Million cell updates/sec
Title: Perfect score: Sequence:	US-09-625-573-1 2232 1 GGATTGAACAAGGACGCATTTATAACTATGTTGATAAAAG 2232
Scoring table: OLIGO_NUC Gapop 60.0	OLIGO_NUC Gapop 60.0 , Gapext 60.0
Searched:	2054640 seqs, 14551402878 residues

Post-processing: Listing first 45 summaries

4109280

Total number of hits satisfying chosen parameters:

Word size :

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	AR116074 Sequence 179542 Sequence 1 U03882 Human monoc 080924 Human monoc AX335952 Sequence U95626 Homo sapien AC096613 Homo sapien G07239 human STS W AR116075 Sequence 3 U03905 Human monoc AX232506 Sequence AX232506 Sequence AX232506 Sequence AX232506 Sequence AX232508 Sequence AX132508 Sequence AX132508 Sequence AF161920 Sequinus AF161921 Sequinus AF161920 Sequinus AF161920 Sequinus AF161920 Sequinus AF161931 Sequinus AF	linear PAT 16-MAY-2001
SUMMARIES th DB ID	2232 6 AR116074 2232 6 179542 2232 6 179542 2232 6 179542 2068 6 AX335952 2068 6 AX335952 2068 1 1 G07239 1068 11 G07239 1079 6 AX116075 1083 6 AX222508 1093 6 AX222508 1019 9 AF161925 1019 9 AF161925 1019 9 AF161925 1019 9 AF161927 1019 9 AF161928 1019 9 AF161928 1019 9 AF161929 1019 9 AF161931 1019 9 AF161903 1019 9 AF161909	2232 bp DNA 1 from patent US 6132987. 1 GI:14096396 1ed. 1 to 2232) 1 to 2232) 2 and Coughlin, S.R. 3 and Coughlin, S.R. 1 (MCP-1R, CCR-2) 15 6132987-A 1 17-OCT-2000;
\$ Result Query No. Score Match Lengt	2232 100.0 2232 100.0 2234 100.0 2232 100.0 2234 100.0 2234 100.0 2234 100.0 2234 100.0 2234 100.0 2234 100.0 2234 100.0 2234 100.0 2234 100.0 2234 100.0 2234 100.0 2234 100.0 2234 100.0 2234 100.0 2234 100.0 2234 100.0 224 10	RESULT 1 AR116074 AR116074 DEFINITION Sequence 1 fro ACCESSION AR116074 1 G. KEYWORDS SOURCE UNKNOWN. ORGANISM UNCLASSITIEG. REFERENCE I (bases 1 t. AUTHORS Charo, I.F. an TITLE RECOMBINAT M. COURNAL PATENT: US 61

E	FEATURES 1 Source 2 S	cat	gani 464	100.0%; Score 2232; DB 6; Length 2232; / 100.0%; Pred. No. 0; .vative 0; Mismatches 0; Indels 0; Gaps	AACGCATTTCCCCAGTACATCCACAACATGCTGCTGCACATCTCGTTCT 6	ATACCAACGAGAGGGGTGAAGAAGTCACCACCTTTTTGATTATGAT 120 	TGACGTGAAGCAAATTGGGCCCCAACTCCTGCCTCCG 18	3TTCATCTTTGGTTTTGTGGCAACATGCTGGTCGTCCTCTTA 24	TGAAGTGCTTGACTGACATTACCTGCTCAACCTGGCCATCTCT 30	TTACTCTCCATTGTGGCTCACTGCTCCAACCTGGCCATCTCT 30 TTACTCTCCCATTGTGGGCTCACTGCTGCAAATGAGTGGGTC 36 TTACTTCTCCATTGTGGGCTCACTGCTGCTGCTTTTTTTT	TGTGCAAATTATTCACGGGGTGTATCACATCGGTTATTTGGGGTC 560 TGTGCAAATTATTCACAGGGCTGATCACATCGGTTATTTTGGCGGA 420 TGTGCAAATTATTCACAGGGCTGTATCACACATCGGTTATTTTGGCGGA 420	CTCCTGACAATGGATAGATACCTGGCTAATGTCCATGCTGTGTT 48	3GTGACAAGTGTGATCACCTGGTTGGTG 54	TGTCCCAGGAATCATCTTACTAATGCCAGAAAGAAGATCTGTT 60	GGAATAATTTCCACACAATAATGAGGAAC 66	CCTGCCGCTGCTCATGGTCATCTGCTACTCGGGAATCCTGAAA 720 	AGAAGAGGATAGGGAGTGAGAGTCATCATCACC 78	TITCICITCIGGACICCCIAIAACATIGICATTCICCTGAACACC 84	CGGCCTGAGTAACTGTGAAAGCACCAGTCAACTGGACCAACCCACG 90	SACTCACTGCTGCATCAATCCCATCATCTATGCCTTC 96
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Charo,I.F. and Coughlin,S.R.
Mammalian monocyte chemoattractant protein receptors and assays
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Molecular cloning and functional expression of two monocyte chemoattractant protein 1 receptors reveals alternative splicing of the carboxyl-terminal tails Proc. Natl. Acad. Sci. U.S.A. 91 (7), 2752-2756 (1994)
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Charo, I.F., Myers, S.J., Herman, A., Franci, C., Connolly, A.J. and Coughlin, S.R.
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Direct Submission
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/COUGL_SCAL_
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/AD_xref="G1:47256"
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VICXSGILKTLLRCRNEKRHRAVRVIFTIMLYYFLFWTPYNIVILLNTFQEFFGLSN
CESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSEFHIALGCRIAPLQKPVCGG
POVRPĞKNYKYTTĞGLLDGRGKĞKSIĞRAPEASLQDKEGA"
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Submitted (01-DEC-1993) Scott J. Myers, Cardiovascular, The Gladstone Institutes, 2550 23rd Street, San Francisco, CA 94110,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 CGGTTTATCAGAAATACCAACGAGGGGGGGAAAGAAGTCACCACCTTTTTGATTATGAT 120
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                                                                                                                                                                 /standard_name="monocyte chemoattractant protein 1
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                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="ccr2-9a"
                                                                                                                                    /clone_lib="MonoMac6-#3"
40. .1164
                                                                                                                      /cell_line="MonoMac 6"
                                              Location/Qualifiers
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HURMCHAUZ 5471 bp DNA linear PRI 24-JUL-1997 Human monocyte chemoattractant protein 1 receptor gene, two alternatively spliced forms, complete cds.
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join(1555. .2546,3756. .5007)
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/note="alternatively spliced form with A-form carboxyl
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                                1741 GITTAATCACATTCGAGTGITTCAGTGCTTCGCAGATGTCCTTGATGCTCATATTGTTCC 1800
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Myers, S.J. and Charo, I.F.
Direct Submission
Submitted (O4-DEC-1996) Pharmacology, Emory University, 1510
Clifton Road, Allanta 30322, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                         1981 AAACACTGGGGCTTCTAGAACCAGGCAACTTGGGAACTAGACTCCCAAGCTGGACTATGGC
                                                                                                  1801 CTAATTTGCCAGTGGGAACTCCTAAATCAAATTGGCTTCTAATCAAAGCTTTTAAAACCCT
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/organism="Homo sapiens"
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                                                                                                         /product="monocyte chemoattractant protein 1 receptor"
//protein_id="AAC51637.1"
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ANEWVFGNAMCKLFTGIYHIGYFGGIFFIILLTIDBYLAINHAYFALKARTYTFGVYT
                                                                                                                                                                                         SVITWINAVEASVPGIIFTKCOKEDSYYVCGPYFPRGWNNFHTIMRNILGLVLPLLIM
VICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLEWTPYNIVILLATFQEFFGLSN
CESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGG
                                                                                                                                                                                                                                                                                                                                            /translation="MLSTSRSRPIRNTNESGEEVTTFEDYDYGAPCHKFDVKQIGAQL
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SVITWINSASVPGIIFTKCOKEDSVYVCGPYFRGWNNFFTIMRNIIGLVLPLLIN
VICYSGILKTLLRCNRIKKRHRAVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSN
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                          'hotem"alternatively spliced form with B-form carboxyl
               /product="monocyte chemoattractant protein 1 receptor"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1159 GCCIAGAGACAGAAATGACAGATCTCTGCTTTGGAAATCACACGTCTGGCTTCACAGATG 1218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGACTCCAGCTGGGTTGGAAAACAGTATTTTCCAAACTACCTTCCAGTTCCTCATTTTTG 1338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AATACAGGCATAGAGTTCAGACTTTTTTAAATAGTAAAAATAAAATTAAAATTAAAGCTGAAAAC 1398
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                                                    join(1606. .2546,3756. .3939)
/note="MCP-1RA receptor; alternatively spliced form
including A-form carboxyl tail"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                           /note="MCP-1RB receptor; alternatively spliced form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1399 TGCAACTTGTAAATGTGGTAAAGAGTTAGTTTGAGTTGCTATCATGTCAAAAGTGAAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1254; DB 9; Length 5471;
                                                                                                                                                                                                                                    PGVRPGKNVKVTTQGLLDGRGKGKSIGRAPEASLQDKEGA"
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100.0%; Pred. No. 0;
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PAT 09-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1519 GTTTGGGAGACTGCTGAGTCAACCCAATAGTTGTTGATTGGCAGGAGTTGGAAGTGTGTG 1578
                                                                4413
                                                                                                                                                                            1639 CAGTATACGCTCCATCGCTGTCATCTCAGCTGGATCTCCATTCTCTCAGGCTTGCTGCCA 1698
                                                                                                                                                                                                 GTTTCAGTGCTTCGCAGATGTCCTTGATGCTCATATTGTTCCCTAATTTGCCAGTGGGAA 1818
                                                                                                                                                                                                                                                                                                                               1819 CICCTAAATCAAATTGGCTTCTAATCAAAGCTTTTAAACCCTATTGGTAAAGAATGGAAG 1878
                                                                                                                                                                                                                                                                                                                                                                                               1939 TICTIATGTTGCCCAGTGTGTTTCTGATCTGATGCAAGCAAGAAACACTGGGGCTTCTAGA 1998
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                                                                                                             1579 ATCTGTGGGCACATTAGCCTATGTGCATGCAGCATCTAAGTAATGATGTCGTTTGAATCA
                                                                                                                                GGCTAAAGAAGGTTTCAGAAAGAAGTGGGGACAGAGCAGAACTTTCACCTTCATATATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCAGGCAACTIGGGAACTAGACTCCCAAGCIGGACIAIGGCTCTACTITCAGGCCACAT
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Horrigan, S., Soppet, D.R. and Weaver, Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTTAACAACTATGATTTGGAAAATAAATCAATGCTATAACTATGTTGATAAAAG 2232
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                                                                                                                                                                                                                                                                                                                                                             1819 CTCCTAAATCAAATTGGCTTCTAATCAAAGCTTTTAAACCCTATTGGTAAAGAATGGAAG 1878
                                                                                                                                                                                                                                                          48553 AGACTCCAGCTGGGTTGGAAAACAGTATTTTCCAAACTACCTTCCAGTTCCTCATTTTG 48612
                                                                                                                                                                                                               1579 ATCTGTGGGCACATTAGCCTATGTGCATGCAGCATCTAAGTAATGATGTCGTTTGAATCA 1638
                                                                                                                                          1459 GCTGTATTAGTCACAGAGATAATTCTAGCTTTGAGCTTAAGAATTTTGAGCAGGTGGTAT 1518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1519 GTTTGGGAGACTGCTGAGTCAACCCAATAGTTGTTGATTGGCAGGAGTTGGAAGTGTGTG 1578
                                                                                                      48253 AGCCTTTTTCACATAGCTCTTGGCTGTAGGATTGCCCCACTCCAAAAACCAGTGTGTGGA 48312
                                                                                                                                                                      1099 CGTGGAAAAGGAAAGTCAATTGGCAGAGCCCCTGAAGCCAGTCTTCAGGACAAAAAGA 1158
                                                                                                                                                                                                                                                                                                       1279 AGACTCCAGCTGGGTTGGAAAACAGTATTTTCCAAACTACCTTCCAGTTCCTCATTTTG 1338
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                                                                                  979 AGCCITTTTCACATAGCTCTTGGCTGTAGGATTGCCCCACTCCAAAAACCAGTGTGTGGA 1038
                                                                                                                            1039 GGTCCAGGAGTGAGACCAGGAAAGAATGTGAAAGTGACTACACAAGGACTCCTCGATGGT 1098
                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                   DB 6; Length 143068;
                                                              2; Indels
/db_xref="taxon:9606"
41194 a 30122 c 32403 g 39349 t
                                                    pred. No. 0;
0; Mismatches
                                          Score 1152;
                                            51.6%;
                                                                  Matches 1252; Conservative
                                                        Similarity
                                              Query Match
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo. Manmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Manmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. D. 1 (bases 1 to 143068)

I (bases 1 to 143068)

NacOmble,W.R., Wilson,R., Chen,E., Gibbs,R., Zuo,L., Johnson,D., Rarall,L., Dedhia,N., Ansari,A., Mardis,E., Schutz,K., Maranabe,M., Doggett,N., Etagcalone,J., Pae,A., Powell,E., Solinsky,K.A., Degjett,N., Garcia,D. and Sagripanti,J.-L. Human BAC clone 110P12

I (bases 1 to 143068)

I (bases 1 to 143068)

Rocomblished (1997)

Rocomble,R.W., Wilson,R., Chen,E., Gibbs,R., Zuo,L., Johnson,D., Rarall,L., Dedhia,N., Ansari,A., Mardis,E., Schutz,K., Gnoj,L., de la Bastide,M., Raplan,N., Greco,T., Touchman,J., Gnoj,L., de la Bastide,M., Kaplan,N., Greco,T., Touchman,J., Porcel,B.M., Dragan,Y., Garcol,M., See,L.H., Tang,M., Porcel,B.M., Dragan,Y., Garcol,C., FitzGerald,M., See,L.H., Tang,M., Porcel,B.M., Dragan,Y., Garcol,C., FitzGerald,M., See,L.H., Tang,M., Porcel,B.M., Dragan,Y., Garcol,C., FitzGerald,M., Yav,Y., Yu,Y., Watanabe,M., Doggett,N., Garcia,D. and Sagripanti,J.-L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chemoattractant protein 1 receptor (ccr2) mRNA (Accession Number U80924), two alternatively spliced mRNAs."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRI 16-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cold Spring Harbor Laboratory, 1Bungtown Rd., Cold Spring Harbor,
NY 11724, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (27-MAR-1997) Advanced Genome Sequence Analysis Course,
                                                                                                                                                                                                                                                                                                                              49393 GTATGATCCTAATGAATGCATAAAATGTTAAGTTGATGATGAAATGTAAATGTTT 49452
2119 GTATGATCCTAATGCATAAAATGTTAAGTTGATGGTGATGAAATGTAAATG 2178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSU95626 143068 bp DNA linear PRI 16-MAY-HOMO Sapiens CCT2D (CCT2), CCT2A (CCT2), CCT5 and CCT6 (CCT6) genes, complete cds, and lactoferrin (lactoferrin) gene, partial cds, complete sequence.
                                                                                                                                                                                         2059 GGCTAAAGAAGGTTTCAGAAAGAAGTGGGGACAGAGCAGAACTTTCACCTTCATATATT 2118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="confirmed by similarity to Human monocyte
                                                                                 1999 ACCAGGCAACTTGGGAACTAGACTCCCAAGCTGGACTATGGCTCTACTTTCAGGCCACAT
                                                                                                                                                                                                                   49453 TITAACAACTAIGATIIGGAAAATAAATGCAATGCTATAACTATGIIGATAAAAG 49506
                                                                                                                                                                                                                                                                                                                                                                                                             2179 IITAACAACTAIGAITIGGAAAATAAAICAAIGCIAIAACTAIGIIGAIAAAAG 2232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Regions with single-strand coverage are as follows:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31434 - 31443 37900 - 37968 53303 - 53357
59166 - 59206 63708 - 63998 65200 - 65335
78605 - 78713 92135 - 92137 112377 - 11251
112643 - 112778 134284 - 134309 134914 - 135019
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:9606'
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095626.1 GI:2104517
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HSU95626
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/note="Identified as a gene by Grail Version 1.3c.
Translated sequence exhibits 42% sequence identity to CCR5
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CSAVFVIGVLDNLLVVLILVKYKGLKRVENIYLLNLAVSNLCFLLTLEFWAHAGGDPW
CKILLGLYFVGLYSEFFFNCLLTVQRYLVFLHKGNFESARRRVPCGIITSVLAWVTAI
LATLPEYVYKPQMEDQKYKCAFSRFPFLPADETFWKHFLTLKMNISYLVLPLFIFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NLDKSVHITKLIATTHCCINPLLYAFLDGTFSKYLCRCFHLRSNTPLQPRGQSAQGTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LYVQMRKTLRFREQRYSLFKLVFAIMVVFLLMWAPYNIAFFLSTFKEHFSLSDCKSSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="DLSDEAERDEYELLCPDNTRKPVDKFKDCHLARVPSHAVVARSV
NGKEDAIWNLLRQAQEKFGKDKSPKFQLFGSPSGQKDLLFKDSAIGFSRVPPRIDSGL
YLGSGYFTALQNLRKSEEEVAARRARVVWCAVGEQELRKCNQWSGLSEGSVTCSSAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YLAVAVYRRSDTSLTRNSVKGKKSCHTAVDRTAGMNIPMGLLFNQTGSCKFDEYFSQS
CAPGSDPRSNLCALCIGDEQGENKCVPNSNERYYGYTGAFRCLAENAGDVAFYKDVTV
LQNTDGNNNDAWAKDLKLADFALLCLDGKRKPVTEARSCHLAMAPNHAVVSRMDKVER
LKQVLLHQQAKFGRNGSDCPDKFCLFQSETKNLLFNDNTECLARLHGKTTYEKYLGPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TEDCIALVLKGEADAMSLDGGYVYTAGKCGLVPVLAENYKSQQSSDPDPNCVDRPVEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     186818"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48253 AGCCTTTTTCACATAGCTCTTGGCTGTAGGATTGCCCCACTCCAAAAACCAGTGTGTGGA 48312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="confirmed by similarity to lactoferrin protein, encoded by GenBank Accession Number M73700, gi 18681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 979 AGCCTTTTTCACATAGCTCTTGGCTGTAGGATTGCCCCACTCCAAAAACCAGTGTGTGGA 1038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1039 GGTCCAGGAGTGAGACCAGGAAAGAATGTGAAAGTGACTACACAAGGACTCCTCGATGGT 1098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1099 CGTGGAAAAGGAAAGTCAATTGGCAGAGCCCCTGAAGCCAGTCTTCAGGACAAAAAAGAAGA 1158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(124605, .>139255)
/gene="lactoferrin"
/gene="lactoferri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="confirmed by similarity to lactoferrin mRNA, accession number M73700"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(join(124782. .124816,126528. .126717,
127884. .128068,130006. .130073,132023. .132164,
133863. .134018,135022. .135075,135890. .135980,
137445. .137599,138436. .138610,139077. .>139253))
/gene="lactoferfin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 143068;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YVAGITNLKKCSTSPLLEACEFLRK" 41194 a 30122 c 32403 g 39349 t
                                                   /evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                             experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="AAB57794.1"
/db_xref="G1:2104521"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="AAB57795.1"
/db_xref="G1:2104522"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="lactoferrin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="lactoferrin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="lactoferrin'
                                                                                                                                                                                                                                                                                                                                                                                                       /product="ccr6"
                                                                                                                                                                                                                                                                                                                                        /codon_start=1
                                                                                    96642. .97676
/qene="ccr6"
                                                                                                                                                           97676
                                                                                                                                                                                                                                                                                                                                                                          /evidence=not_
                                                                                                                                                                                        /gene="ccr6"
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                                                                                                                                                                                                                                                                                                       protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="AAB57791.1"
/db_xref="G1:2104518"
/translation="MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQL
LPPLYSLVFIFGFYGNMLVVLILINCKKLKCLTDIYLLNLAISDLEFLITLPLWAHSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANEWPEGNAMOKLETGELYHIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVT
SVITWLVAVFASVPGIIFTKOQREDSYYVCGPYFPRGWINFHTIMRNILGLVLPLLIM
VICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWTPYNIVILNTFORFFGLSN
CESTSOLDQATQVTFFIGMTHCCINPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGG
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ANEWVEGNAMCKLFTGLYHIGYFGGIPFILLITDRYLAIVHAVEALKARTVTFGVYA
ANEWVEGNAMCKLFTGLYHIGYFGGIPFILLITLETDRYLAIVHAVEALKARTVTFGVYA
VCYSGTIKTLLACKOKEDSYVGCPFPRGWNNRHTIMRNILGIYLPLILM
CESTSGLDQATGVTETLGMTHCCINPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPV
59531. . 64785
/gene="ccr5"
join(59531. . 59573, 61472. . 64785)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="AAB57792.1"
/db_xref="G1:2104519"
/translation="MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="AAB57793.1"
/db_xref="G1:2104520"
/translation="MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LPGIIFTRSQKBGLHYTCSSHFPYSQYQFWKNFQTLKIVILGLVLPLLVWYICYSGIL
KTLLRCRNEKKRHRAVRLIFTIMIVYFLFWARYNIVLLLNTFQEFGLNNCSSSNRLD
QAMOYTETLGMTHCCINPIIYAFVGEKFRNYLLVFFQKHIAKRFCKCCSIFQQBAPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FVGNMLVILILLINCKRLKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQ
LLTGLYFIGFFSGIFFIILLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVYAVFAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /hote="Putative mRNA identified by homology to CCR5 mRNA."
                                                                                                                                                                                                                                                                                                                                                                                                    chemoattractant protein 1 receptor (ccr2) alternatively spliced mRNA encoding B-form carboxyl tail. Accession Number: U80924."
                                                                                                                                                                         alternatively
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chemoattractant protein 1 receptor (ccr2) alternatively spliced A-form, Encoded by GenBank Accession Number U80924, gi 1168965"
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                                                                                                                      /note="confirmed by similarity to Human monocyte chemoatractant protein 1 receptor (ccr2) alternativel spliced mRNA encoding A-form carboxyl tail, Accession Number U80924."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="confirmed by similarity to Human monocyte chemoattractant protein 1 receptor (ccr2), Accession Number: 1168965"
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                                                                                                                                                                                                                                                                                                                                                           /note="confirmed by similarity to Human monocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                join(46106...47046,48255...48438)
/gene="ccr2"
/note="confirmed by similarity to Human monocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ccr5) mRNA. Accession number: U54994.
јотп(46056. .47046,48255. .49505)
/gene≂"ccr2"
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/gene="ccr5"
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                                                                                 /product="ccr2a"
                                                                                                                                                                                                                                                                                                                                     /product="ccr2b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="ccr2a"
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/product="ccr6"
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/gene="ccr2"
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49333 GGCTAAAGAAGGTTTCAGAAAGAAGTGGGGACAGAGCAGAACTTTCACCTTCATATTT 49392
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                                                                                                                                                                                    2119 GTATGATCCTAATGAATGCATAAAATGTTAAGTTGATGGTGATGAAATGTAAATACTGTT 2178
                                                                                                                                        GIGGAGAAGCICCCIGAAGIAAGCAAAGACIIICCICITAGICGAGCCAAGIIAAGAAIG 1938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1939 TICITAIGIIGCCCAGIGITITCIGAICIGAIGCAAGCAAGAAACACIGGGCIICIAGA 1998
                                                                                                                                                                                                                                                                                                                                              1699 AAAGCCTTTTGTGTTTTTGTATCATTATGAAGTCATGCGTTTAATCACATTCGAGT 1758
                                                                                                                                                                                                                                                                                                                                                                                                                                CICCIAAAICAAAIIGGCIICIAAICAAAGCIIIIAAACCCIAIIGGIAAAGAAIGGAAG 1878
                                         AGACTCCAGCTGGGTTGGAAAACAGTATTTTCCAAACTACCTTCCAGTTCCTCATTTTG 1338
                                                                                                                                                                       GCTGTATTAGTCACAGAGATAATTCTAGCTTTGAGCTTAAGAATTTTGAGCAGGTGGTAT 1518
                                                                                                                                                                                                                                                           1579 ATCTGTGGGCACATTAGCCTATGTGCATGCAGCATCTAAGTAATGATGTCGTTTGAATCA 1638
                                                                                                                                                                                                                                                                                                    1639 CAGIATACGCTCCATCGCTGTCATCTCAGCTGGATCTCCATTCTCTCAGGCTTGCTGCCA 1698
                                                                                    AATACAGGCATAGAGTTCAGACTTTTTTAAATAGTAAAAATAAAATTAAAAGCTGAAAAC 1398
                                                                                                                               TGCAACTTGTAAATGTGGTAAAGAGTTAGTTTGAGTTGCTATCATGTCAAACGTGAAAAT 1458
49393 GTATGATCCTAATGAATGCATAAAATGTTAAGTTGATGGTGAAGTGTAAATACTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2179 ITTAACAACTATGATTTGGAAAATAAATCAATGCTATAACTATGTTGATAAAAG 2232
             1879
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases I to 185437) (kaul.R.K., Olson, M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z., Saenphimmachak,C., Phelps,K.A., Buckley,D., Kibukawa,M., Raymond,C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,
Saenphimmachak, C., Phelps, K.A., Buckley, D., Kibukawa, M., Raymond, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (01-AUG-2002) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA on Aug 1, 2002 this sequence version replaced gi:16445164.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (26-OCT-2001) Genome Center, University of Washington,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence has been validated by Multiple Complete Digest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5': BAC-110P12 U95626, 111014-bp overlap
3': RP11-509121 (UMGC:bc0454) AC104304, 61294-bp overlap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center clone mame: RP11.24F11 (bc0137)
Center clone mame: RP11.24F11 (bc0137)
Sequencing vector: plasmid; L08752; 100% of reads Chemistry: Dye-terminator ET; 93% of reads Assembly program: Phrap; version 0.990319
Consensus quality: 184860 bases at least 040
Consensus quality: 185398 bases at least 020
Consensus quality: 185395 bases at least 020
Insert size: 185437; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality quality levels above 40 are expected to have less than 1 error in 10,000 bp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality coverage: 7.6x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center: University of Washington Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 185437)
Kaul,R.K., Olson,M.V., Raymond,C. and Haugen,E.D.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://www.genome.washington.edu
Contact: uwgchtgs@u.washington.edu
------- Project Information
Center project name: chr.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Box 352145, Seattle, WA 98195, 3 (bases 1 to 185437)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence Quality Assessment:
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AC098613
AC098613.2 GI:22038607
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Direct Submission
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                                                                                                                                                                                                                                                                                                              and Haugen, E.D
                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                     Unpublished
                                                                                              human.
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JOURNAL
                                                                                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                           TITLE
JOURNAL
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                                                                                              SOURCE
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fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC.

PRI 01-AUG-2002

linear

Homo sapiens chromosome 3 clone RP11-24F11, complete sequence.

185437 bp

AC098613

DEFINITION

RESULT 7 AC098613

0 14921 14985 6	'	, ,	0 2159 2172	3 3573 3564	0 5252 5237			7 1565 1603	5 1645 1603	573 <800	3 7986 7830	7 2313 2324	49 <800	125	2290 2324	205	; ; ; ; ;								Length 185437;	sdr	AAAAACCAGTGTGTGA 1038 	1098		FTCAGGACAAAGAAGGA 1158	163	FTTGGCTTCACAGATG 1218
1109 1130	6383 6450	332 · <800	242 <800	15571 15803	453 <800	1429 1394	655 <800	7881 7987	7533 7635	585 <800	2998 2973	8796 8837	1331 1304	7102 7161								alifiers	/organism="Homo sapiens" /db_xref="taxon:9606"	="3" 1-24F11"	core 1101; DB 9	0; Mismatches 3;		GAATGTGAAAGTGACTACACA		CAGAGCCCTGAAGCCAGTCT	CAGAGCCCTGAAGCCAGTCT	CICIGCITIGGAAAICACACC
193 <800	2546 2640		9190 9107	352 <800	1157 1161	3967 3953	1369 1334	752 752	. 1624 1653	3258 3381	9624 9684	2841 2870	2979 3069	3898 3953	4830 4804	2418 2459	6198 6066	534 <800	3985 3953	1184 1161	63 <800	Location/Qualifier 1185437	/organism="F /db_xref="te	/chromosome= /clone="RP11	Query Match Best Local Similarity 99.8%;	51; Conservative	AGCCTTTTTCACATAGCTCTTGGCTTAGGATTGCCCCACTCCAAAACCAGTGTGGGAAAACCAGTGTGGGAAAACCAGTGTTTTAGAAAAACAGAGTGTTGGAAAAAAAA	GGTCCAGGAGTGAGACCAGGAAAGAATGTGAAAGTGACTACACAAGGACTCCTCGATGGT		CGTGGAAAAGGAAAGTCAATTGGCAGAGCCCCTGAAGCCAGTCTTCAGGACAAAGAAGGA	CGTGGAAAAGGAAAGTCGAAGGAGCCCCTGAAGCCAGTCTTCAGGACAAAGAAGA	occinomanchomming to the control of
																						FEATURES Source			Query Match Best Local	Matches 12:	16204	QY 1039 GG1	Db 16264 GGT	1099	Db 16324 CGI	16384
y 400–800 bp) appear repancies 1y ordered	111	FngrPrnt		9423	6501	<800	<800	6501	10229	1025	3176	1025	3998	1025	<800	2693	1968	<800	7474	1267	1025	3301	5237	6926	<800 2576	2172	3802	7830	16442	10820	1968	4815
variable cutoff (approximately 400-800 fingerprint and hence do not appear no significant remaining discrepancies and predicted values. Uniquely ordere	Hind	SeqDerMap		9531		512	449	6692	10449	953	3124	1054	3985	1100	124	2671	1948	83	7455	1305	1047	3299	5279	6815	435	2218	3797	7758	16192	11020	1976	4795
variable cutoff (fingerprint and hosignificant read predicted value for the forest for the forest form of the forest fore	RI LINES.	FngrPrnt		8837	<800	1824	3986	1130	<800	<800	2267	4891	3078	1394	9772	1021	12503	898	9772	3601	<800	7635	2075	5858	3986	1928	3986	2771	<800	13328	2450	2267
s below a variable red in the fingerpri There are no signii retimental and preciperated by assivation	ECORI	SeqDerMap		9698	9	1846	4052	1159	54	260	2287	4905	3049	1377	6066	1022	12606	866	9817	3598	452	7549	2063	5837	4104	1943	3964	2758	167	1307	2423	2243
Small fragments below a vare not resolved in the in the table. There are not between the experimental fragments are separated?		Pr		12040	2065	5720	3953	897	897	2215	1653	5720	5720	5001	2640	<800	1161	5720	9684	666	4503	2981	<800	3602	<800	10140	1452	<800	<800	9684 3953	1234	3381
Small fra are not r in the ta between t	Bglii	SeqDerMap	:	11786	2067	5681	3716	875	910	2169	705	5763	5844	5061	2625	725	173	5747	9995	666	4541	2950	406	3375	416	10298	1478	287	205	3809	1275	3351

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17344 GTATGATCCTAATGAATGCATAAAATGTTAAGTTGATGGTGATGAAATGTAAATACTGTT 17403
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                                                                             1819 CTCCTAAATCAAATTGGCTTCTAATCAAAGCTTTTAAACCCTATTGGTAAAGAATGGAAG 1878
                                                   1699 AAAGCCITTTGTGTTTTGTTTTGTATCATTATGAAGTCATGCGTTTAATCACATTCGAGT 1758
          1639 CAGTATACGCTCCATCGCTGTCATCTCAGCTGGATCTCCATTCTCTCAGGCTTGCTGCCA 1698
                                                                                                                                                             GCTGTATTAGTCACAGAGATAATTCTAGCTTTGAGCTTAAGAATTTTGAGCAGGTGGTAT 1518
                                                                                                                                                                                                     1519 GITTGGGAGACTGCTGAGTCAACCCAATAGTTGTTGATTGGCAGGAGTTGGAAGTGTGTG 1578
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                                        1279 AGACTCCAGCTGGGTTGGAAAACAGTATTTTCCAAACTACCTTCCAGTTCCTCATTTTG 1338
1999 ACCAGGCAACTTGGGAACTAGACTCCCAAGCTGGACTATGGCTCTACTTTCAGGCCACAT
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STS 19-0CT-1995

linear

human STS WI-9314, sequence tagged site.

G07239

LOCUS

RESULT 8

1068 bp

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         G07239.1 GI:860484
STS; STS sequence; primer; sequence tagged site.
Homo sapiens STSS derived from sequences in dbEST and the Unigene
                                                                             Eukaryota. Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1068)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1285 CAGCIGGGTIGGAAACAGIATITICCAAACIACCITCCAGITCCICAITITIGAAIACA 1344
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1. 1068
/dorganism="Homo sapiens"
/do_xref="taxon:9666"
/map="730_D_5; 913_C_5; 941_A_7; 743_H_10; 781_B_10;
881_F_10; 881_F_11"
                                                                                                                                         Whitehead Institute/MIT Center for Genome Research; Physically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Prepared with primer pairs derived from U03882 -- Unigene.
Location/Qualifiers
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                                                                                                                                                                                                                        Whitehead Institute/MIT Center for Genome Research
Whitehead Institute for Biomedical Research
                                                                                                                                                                                                                                                 9 Cambridge Center, Cambridge MA 02142 USA
Tel: 617 252 1900
Fax: 617 252 1902
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.025 units/ul
                                                                                                                                                                                                                                                                                                       Email: thudson@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(121. .140)
1 186 c 238 g
                                                                                                                                                                                                                                                                                                                                                     Primer B: ACTGTTTTCCAACCCAGCTG
                                                                                                                                                                                                                                                                                                                                      Primer A: GGAAATCACACGTCTGGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                Denaturation:
Annealing: 56 degrees C
Polymerization:
                                                                                                                                                                                                              Contact: Thomas Hudson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCR Cycles: 35
Thermal Cycler:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dNTPs: each 4 nm
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KC1: 50 mM
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PCR Profile:
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1405 TIGIAAATGIGGIAAAGAGTTAGTTIGAGTTGCTATCAIGTCAAACGIGAAAAIGCIGIA 1464
                                                                         TTAGTCACAGAGATAATTCTAGCTTTGAGCTTAAGAATTTTGAGCAGGTGGTATGTTTGG 1524
                                                                                                             GAGACTGCTGAGTCAACCCAATAGTTGTTGATTGGCAGGAGTTGGAAGTGTGTGATCTGT 1584
                                                                                                                                               1585 GGGCACATTAGCCTATGTGCATGCAGCATCTAAGTAATGATGTGGTTTGAATCACAGTAT 1644
                                             ACGCTCCATCGCTGTCATCTCAGCTGGATCTCCATTCTCTCAGGCTTGCTGCCAAAAGCC 1704
                                                                                                                                                                                                                        TITIGICITITGITITGIATCATTATGAAGTCATGCGITTAATCACAITCGAGTGTTTCA 1764
                                                                                                                     1765 GICCTICGCAGAIGICCTIGAIGCICAIAITGIICCCIAAIITIGCCAGIGGGAACICCIA 1824
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PAT 16-MAY-2001
                           linear
                           DNA
                     Sequence 3 from patent US 6132987.
AR116075
AR116075.1 GI:14096397
                                                                                                     (bases 1 to 1979)
                                                                                          Unclassified
                                                                      Unknown.
                                                                                 Unknown
                              DEFINITION
                                                                                ORGANISM
RESULT 9
AR116075
                                         ACCESSION
                                                                                                    REFERENCE
                                                              KEYWORDS
                                                  VERSION
                    LOCUS
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61 CGGTTTATCAGAAATACCAACGAGAGCGGTGAAGAAGTCACCACCTTTTTGATTATGAT 120
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                                                                                                                                                                                                                         Gaps
                                                                                                                                              241 ATAAACTGCAAAAAGCTGAAGTGCTTGACTGTACTTTACCTGCTCAACCTGGCCATCTCT 300
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                                                                                                                                                                                                                                                                                                                                                                            420
                                                                                                                                                                                                                                                                                                                                                                                                                 480
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Recombinant nammalian monocyte chemotactic protein-1 (MCP-1)
receptors (MCP-1R, CRC-2)
Patent: US 6132987-A 3 17-OCT-2000;
Location/Qualifiers
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Molecular cloning and functional expression of two monocyte chemoattractant protein 1 receptors reveals alternative splicing of the carboxyl-terminal tails
Proc. Natl. Acad. Sci. U.S.A. 91 (7), 2752-2756 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1979)
Charo,I.F., Myers,S.J., Herman,A., Franci,C., Connolly,A.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (02-DEC-1993) Scott J. Myers, Cardiovascular, The Gladstone Institutes, 2550 23rd Street, San Francisco, CA 94110,
                                                                                                                                                                                                                                               721 ACCTGCTTCGGTGTCGAAACGAGAAGAAGAGGCATAGGGCAGTGAGTCATCTTCACC 780
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/standard_name="monocyte chemoattractant protein 1
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                                 /note="alternatively spliced; MCP-1RB"
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/protein_id="AAA19120.1"
/db_xref="G1:472558"
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/db_xref="taxon:9606"
/clone="ccr2-2a"
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Direct Submission
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Location/Qualifiers
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Charo, I.F. and Coughlin, S.R.
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/translation="MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKOIGAQL
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ANBWYFGNWARCKLFTGLYHIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVT
SVITWLVANAWFASVPGIFFTKGKEDSVYVCGPFFRGWNFFTIRNTLAIGLYLPLLL
VICYSGILKTLLRCRNFKKRHRAVRVTFTIMTYYFLWTPYNIVILLINTEGBFFGLSN
CESTSQLDQATQYTFTLGMTHCCINPIIYAFVGKFRRYLSVFFRKHITKRFCKQCPV
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1083) (bases 1 to 1083) (bases A.M., Groot, P.H. and Spurr, N.K. CCr2-641, polymorphic variant of the human ccr2 receptor and its use in the diagnostic and treatment of atherosclerosis SMITHKLINE BEECHAM PLC (GB)
121 GGGGCCCAACTCCTGCCTCCGCTCTACTCGCTGTTCATCTTTGGTTTTGTGGGCAAC 180
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/db_xref="taxon:9606"
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81 ATCATGATTGTTTACTTTCTCTTCTGGACTCCCTATAACATTGTCATTCTCCTGAACACC 840

762 ACCCTGCTTCGGTGTCGAAACGAGAAGAAGAGGCATAGGGGAAGTGAGAGTCATCTTCACC

841 TTCCAGGAATTCTTCGGCCTGAGTAACTGTGAAAGCACCAGTCAACTGGACCAAGCCACG 900

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280 CIGCICAACCIGGCCAICICIGAICIGCITITICITAITACICICCCAITGIGGGCICAC
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I (bases 1 to 1083)
Valdes,A.M., Groot,P.H. and Spurr,N.K.
Ccr2-64i, polymorphic variant of the human ccr2 receptor and its was in the diagnostic and treatment of atherosclerosis patent: WO 0162796-A 30-AUG-2001;
SMITHKLINE BEECHAM PLC (GB)
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            580 TGCCAGAAAGAAGATTCTGTTTATGTCTGTGGCCCTTATTTTCCACGAGGATGGAATAAT 639
                         ITCCACACACAATAATGAGGAACATTTTGGGGCTGGTCCTGCCGCTGCTCATCATGGTCATC 699
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Pred. No. 0;
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Sequence 1 from Patent WO0162796.
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Best Local Similarity 99.9%;
Matches 940; Conservative
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Human mRNA for monocyte chemoattractant protein 1 receptor (MCP-1
receptor), complete cds.
D29984
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G-protein-coupled seven-transmembrane-type receptor; MCP-1 receptor; monocyte chemoattractant protein 1 receptor. Homo sapiens monocyte cell-line THP-1 cDNA to mRNA. Homo sapiens
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340 TCTGCTGCAAATGAGTGGGTCTTTGGGAATGCAATGTGCAAATTATTCACAGGGCTGTAT
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Blochem. Biophys. Res. Commun. 202 (2), 1156-1162 (1994)
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/translation-"MLGTSRSRPIRNTNESGEBYTFFDYDYGAPCHKFDVKGIGAQL
LPPLYSLYFTGFFGFWYDTLINGKKLKOLTDIYLLNLAJSDLLFLITLPLWAHSA
LPPLYSTETTGFFTGFYTTGYFGGIFFTILLTIDIYLALIWAYNTALLERRTVTFGVYT
SVITWLVAVFASVPGIIFTKORGESVYVCGPFFRGWNNFHTIMNTIGLYLPLLIN
CLSTSGLIKTLLRCRWERKRAVNVIFTIMNTYFLEWTPYNIVILLNTFQEFFGLSN
CESTSQLDQATQVFTFGMTHCCINPIIAFVGEKFRRYLSVFFRKHTIKRFCKQCPV
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             Direct Submission
Submitted (22-APR-1994) Shinsuke Yamagami, TELJIN LIMITED,
1915 Institute for Bio-Medical Research; 4-3-2 Asahigaoka, Hino, Tokyo
Submitted (22-Apr-1994) to DDBJ by:
                                                                                                                                                                                                                                                                                             /product="Monocyte Chemoattractant Protein 1 Receptor"
/protein_id="BAA06253.1"
/db_xref="G1:531247"
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                                                                                          Teijin Limited
Institute for Bio-Medical Research
4-3-2 Asahigaoka
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/cell_line="THP-1"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Non-endogenous, consstitutively activated known g protein-coupled
481 AGTGTGATCACCTGGTTGGTGGCTGTTTGCTTCTGTCCCAGGAATCATCTTTACTAAA 540
                                     640 ITCCACACAATAATGAGGAACATTTTGGGGCTGGTCCTGCCGGTGCTCATCATGGTCATC 699
                                                                                     700 IGCTACICGGGAAICCIGAAAACCCIGCIICGGIGICGAAACGAGAAGAAGAGGCAIAGG 759
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                         580 IGCCACAAAGAAGATTCTGTTATGTCTGTGGCCCTTATTTTCCACGAGGATGGAATAAT
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